SEQUENCE LISTING

<110> OriGene Technologies, Inc.

<120> Human Tbx20 Gene and Uses

<130> 18U 101 R1

<160> 3

<170> PatentIn version 3.0

<210> 1
<211> 6717
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (462)..(1805)

<400> 1

```
gcgccgcgct ccccacgcca gcgtcctagc agccgcgctc ggctggtggc cacctcagcc        60

tgggacatcc cggctgtccc cagccccaga gggaggaagg acgcggaggg gatgctccag       120

gaccccagga ctttgtgcag ttgatgctcg tttccgcctt cgggctgtgc agactgtcgt       180

cctgccgagc gccccggggc gtgcgcaccc gccgtagtgc tcggtgggcc ctctcctctc       240

cggctgcctt cgaagtctct gcggctctgg ggctttgcgg tggggaatag aggccagtgt       300

gcagctctgg agtcgttgga gctgacactt ctggagtccc tggccccgct gtgactgctc       360

tcggaaactt tgagctgtgt ttcgggtctt tgtctccctt ggggaatctg gacggcagtt       420

cggacgaccc cgtccctggc caggaccgcg tgctggggac c atg gag ttc acg gcg       476
                                            Met Glu Phe Thr Ala
                                            1               5
```

```
tcc ccc aag ccc caa ctc tcc tcc cgg gcc aac gcc ttc tcc att gcc       524
Ser Pro Lys Pro Gln Leu Ser Ser Arg Ala Asn Ala Phe Ser Ile Ala
            10                  15                  20

gcg ctc atg tcg agc ggc ggc tct aag gag aag gag gcg acg gag aac       572
Ala Leu Met Ser Ser Gly Gly Ser Lys Glu Lys Glu Ala Thr Glu Asn
            25                  30                  35

aca atc aaa ccc ctg gag caa ttt gtg gag aag tcg tcc tgt gcc cag       620
Thr Ile Lys Pro Leu Glu Gln Phe Val Glu Lys Ser Ser Cys Ala Gln
            40                  45                  50

ccc ctg ggt gag ctg acc agc ctg gat gct cat ggg gag ttt ggt gga       668
Pro Leu Gly Glu Leu Thr Ser Leu Asp Ala His Gly Glu Phe Gly Gly
        55                  60                  65

ggc agt ggc agc agc ccg tcc tcc tcc tct ctg tgc act gag cca ctg       716
Gly Ser Gly Ser Ser Pro Ser Ser Ser Ser Leu Cys Thr Glu Pro Leu
70                  75                  80                  85

atc ccc acc acc ccc atc atc ccc agt gag gaa atg gcc aaa att gcc       764
Ile Pro Thr Thr Pro Ile Ile Pro Ser Glu Glu Met Ala Lys Ile Ala
                90                  95                  100

tgc agc ctg gag acc aag gag ctt tgg gac aaa ttc cat gag ctg ggc       812
Cys Ser Leu Glu Thr Lys Glu Leu Trp Asp Lys Phe His Glu Leu Gly
            105                 110                 115

acc gag atg atc atc acc aag tcg ggc agg agg atg ttt cca acc atc       860
Thr Glu Met Ile Ile Thr Lys Ser Gly Arg Arg Met Phe Pro Thr Ile
            120                 125                 130

cgg gtg tcc ttt tcg ggg gtg gat cct gag gcc aag tac ata gtc ctg       908
Arg Val Ser Phe Ser Gly Val Asp Pro Glu Ala Lys Tyr Ile Val Leu
```

```
                 135                    140                   145
     atg gac atc gtc cct gtg gac aac aag agg tac cgc tac gcc tac cac      956
     Met Asp Ile Val Pro Val Asp Asn Lys Arg Tyr Arg Tyr Ala Tyr His
     150                     155                   160                 165

     cgg tcc tcc tgg ctg gtg gct ggc aag gcc gac ccg ccg ttg cca gcc     1004
     Arg Ser Ser Trp Leu Val Ala Gly Lys Ala Asp Pro Pro Leu Pro Ala
                         170                   175                 180

     agg ctc tat gtg cat cca gat tct cct ttt acc ggt gag caa cta ctc     1052
     Arg Leu Tyr Val His Pro Asp Ser Pro Phe Thr Gly Glu Gln Leu Leu
                     185                   190                   195

     aaa cag atg gtg tct ttt gaa aag gtg aaa ctc acc aac aat gaa ctg     1100
     Lys Gln Met Val Ser Phe Glu Lys Val Lys Leu Thr Asn Asn Glu Leu
                 200                   205                   210

     gat caa cat ggc cat ata att ttg aac tca atg cat aag tac cag cca     1148
     Asp Gln His Gly His Ile Ile Leu Asn Ser Met His Lys Tyr Gln Pro
             215                   220                   225

     agg gtg cac atc att aag aag aaa gac cac aca gcc tca ttg ctc aac     1196
     Arg Val His Ile Ile Lys Lys Lys Asp His Thr Ala Ser Leu Leu Asn
     230                   235                   240                 245

     ctg aag tct gaa gaa ttt aga act ttc atc ttt cca gaa aca gtt ttt     1244
     Leu Lys Ser Glu Glu Phe Arg Thr Phe Ile Phe Pro Glu Thr Val Phe
                     250                   255                   260

     acg gca gtc act gcc tac cag aat caa ctg ata acg aag ctg aaa ata     1292
     Thr Ala Val Thr Ala Tyr Gln Asn Gln Leu Ile Thr Lys Leu Lys Ile
                     265                   270                   275

     gat agc aat cct ttt gcc aaa gga ttc cgg gat tcc tcc agg ctc act     1340
     Asp Ser Asn Pro Phe Ala Lys Gly Phe Arg Asp Ser Ser Arg Leu Thr
                 280                   285                   290

     gac att gag agg gaa agt gtg gag agc ctg att caa aag cat tcc tat     1388
     Asp Ile Glu Arg Glu Ser Val Glu Ser Leu Ile Gln Lys His Ser Tyr
     295                   300                   305

     gca cgc tca ccc atc cgt acc tac gga gga gaa gaa gat gtc ttg ggg     1436
     Ala Arg Ser Pro Ile Arg Thr Tyr Gly Gly Glu Glu Asp Val Leu Gly
     310                   315                   320                 325

     gat gag agt cag aca acc cca aat cga ggg tca gcc ttt aca aca tct     1484
     Asp Glu Ser Gln Thr Thr Pro Asn Arg Gly Ser Ala Phe Thr Thr Ser
                     330                   335                   340

     gat aat ttg tct ctc agc tcc tgg gta tca tct tct tcc agt ttt cct     1532
     Asp Asn Leu Ser Leu Ser Ser Trp Val Ser Ser Ser Ser Phe Pro
                     345                   350                   355

     ggg ttt cag cac cca cag tcc ctg act gct ctt ggc acc agc aca gca     1580
     Gly Phe Gln His Pro Gln Ser Leu Thr Ala Leu Gly Thr Ser Thr Ala
                     360                   365                   370

     tcc ata gca aca ccc att cct cac ccc atc cag ggt tct ctg cca cca     1628
     Ser Ile Ala Thr Pro Ile Pro His Pro Ile Gln Gly Ser Leu Pro Pro
             375                   380                   385

     tat agc cga ctg gga atg cct ctg aca cca tcg gcc att gcc agc tcc     1676
     Tyr Ser Arg Leu Gly Met Pro Leu Thr Pro Ser Ala Ile Ala Ser Ser
     390                   395                   400                 405

     atg caa ggg agt ggc ccc aca ttc cct tca ttc cac atg ccg cga tac     1724
     Met Gln Gly Ser Gly Pro Thr Phe Pro Ser Phe His Met Pro Arg Tyr
                     410                   415                   420

     cat cac tat ttt cag cag ggg ccc tat gct gcc att caa gga cta cgc     1772
     His His Tyr Phe Gln Gln Gly Pro Tyr Ala Ala Ile Gln Gly Leu Arg
                     425                   430                   435
```

```
cat tcc tct gct gtg atg acg cca ttt gta tga ctcttctaaa aatgggagaa   1825
His Ser Ser Ala Val Met Thr Pro Phe Val
        440                 445

tccagatcca gaatgtgcaa gtgggtatgg aaatatagga cagggctggg tgggtgggat   1885

gtggggtatc ggagcagggg ctttccagga gacacaggac ctatcaaaga ggagagccag   1945

actcacaata aaacctacca ctgagggaat gcaccacgga ccaggattca tctgagggac   2005

agctcttggg ttcaggagag aatccatgta aagttctcag ccagcctgaa agtttactaa   2065

tacaaggctg atgaatctta aagtgcatta ttcctcatgg ttaaaacgct gtgttcatgc   2125

agtaatgtat aaaatcattg tgtgtagggt ttcttcctgc ttttcacagg ataaaagaat   2185

cttcaaagag gccatactat atagcatact gaccataatg actaactgaa gtcaatttat   2245

ccctgtagaa aatgggagcc agtagagaaa tatttgtagt gctgtagcat aagcatgttt   2305

agttttcttt tatgttagtc tgctggggaa ggagctgaga taatgctaat gcatcctgtt   2365

ttgtggatga atacacggta atgacctcac aaagttctgt ttgtaatatt gaagggccag   2425

taaccaataa gctcagtttt cacagtcttc tttcttccta gttctcttta ttgcaaatac   2485

ttgccagagt tagggttggg gctagagtta tggaggaaaa atcttccata tacagttttg   2545

aagcaagagc ctctctatat tacacggtaa aactgaagtt tgatttttct gggctgcatt   2605

ctaaacacac tactgactaa ttcactgagg aacactccaa agcctaggca tgatgttatg   2665

tgaggctcgc tttcacttac agctgcaaca gaaggatggt tgttctattc cagaaggatt   2725

tctctgccgt tggtgccaga gatcccttca ttttcacttc agttttggaa gaccttgtgg   2785

atgttaaaat gcatctggac aaattctcat tttcagtaaa tctgctttgt tgttgctgcc   2845

gctgattgac aaggatttga gaatgaccat tctaaatgcc aggatagcca tgatttaact   2905

tatgttcctg agtggaaatg tgtccataca tctaatttgg ccttttttcct tactgtgtta   2965

catttagtga ctcctttacc attttgctag gtctgtaatc ttaaattgct tgataatgga   3025

atggctccat aactgaaatg ttggcaattc ttataagtaa tctaaagcat tcttccactt   3085

tattttcaac ttttgctatc ttcttaagcc ttcctttaat gtttataata gtaacaaata   3145

ttttagttat atatgacctg tatattgttt ttgaacagca tatatatata tatatatatg   3205

catttacagt cagggtaaca catttggcat tttgcaacaa tttatttccc taataacata   3265

gttttaatga aattaatagt ttttcaactt tagatttaat gcacttcaac tacaggatgc   3325

aacctgtcgt cttagaaaat ttctccaaaa ctctaattta atttttatat gtaatattca   3385

ttctactctt cttgctacaa aagtattgaa tctgttaaaa gggatgggaa atatttctac   3445

tgacagtaga agtgtatttg gggggaaatg caatatactt atcacatcag actcccgtgg   3505

gattttattt ggtggtttta atgttagcct ttttcatatc acatgccttt ctgggcactt   3565

ccagcttgtg aaacaaggca tcatggcaca gcctgtctag gtgatgctgt tgttggattt   3625

tgcccttgct attctccact gtactccaaa gtttacttac agaaaagcat gggctgcgtt   3685

aacaaagcat ctcacgatcc tacagcaaac actgtgggcc aatttttaac ttgttgcatg   3745

ttatgctgta gtatccatag gtagtttgtt ttcaaacaaa gtacaggtgt gcatttcttt   3805

aaaaaagcag ttatgagtaa tgtttaaact atccatagag ctaggatagg ggtttactat   3865

ttaatagctg gcctgttgcc agtgctcctt tgaatataga gtactgctgc ttaaagcagg   3925
```

```
aataacaaaa gatgctgttt tacataaggc tactcaatac cctgataaat tactggtcta   3985

ctaaggtgaa tctgtatctg aattttattt tcaaagagga tgaaaagatt gttttaatac   4045

atactgtttt gacatttcta ccaatctgtg tgtctcaaag agatttgtgt gtttttgttg   4105

aatatggttt tacctagtat ttcctgactt cataatttta ttttgtaatt aagcaatata   4165

agactataaa taagagtgct tagagaaaac aaagactagt cagacctaaa attctaaatt   4225

gggtatatat ttttaagtat tattcgaacc agagaaaaga agcacaagtg aaatagagct   4285

taacctcatc agagtcactt gatccatgga aaccaagggg tagaaatttc ccctccctgg   4345

gcctttctga ggtatcctgg tcattgattc ttattaaacc cttgggagtt tagtatttaa   4405

aattccaaag cccattctgg caaaagtaat ttcaagaact acctatttaa tgggaaagcc   4465

aattgaataa taaaggccat gaattataat atatttagaa tatattcagg gttcctccca   4525

cgactccccc cgcccccga gtatattata gtgtcaaaaa gcatggctaa tgggaagtgc   4585

tgctaaaaag aggtcctgcc agacctgctt tatctaatcc tgaggaatta attcagaact   4645

taataggttt tgcagttgtg gtttgttttt aaaatatcaa taattctgag tagattcaag   4705

gtcttttttt tgttttgttt tgttttgttt tgtttttgag acggagtctc actctgttgc   4765

taggctagag tgcagtggca tgatctcggc tcactgtaac ctccgtctcc tgggttcaag   4825

caattctcct gcctcagccc cctgagtagc taggattaca ggtgtgcgct accatgccca   4885

gctaatttta gtatttttag tagagacagg atttttaccat gttggccaag atggtctcga   4945

tctcttaacc ttctgatcca cccacctcgg cctcccaaag tgctgggatt acaggcatga   5005

gccaccacac ccggcctcaa tttttttttt tttttttttt tttttttttac taacttagtc   5065

ttctcctctc ctctgtctac ccttagcaat atataggtaa acatatccag cttgtctaac   5125

acatcacaga ttattagtta acaaggtgta gattaatgag cttatattgt attgctggat   5185

cttttgagtt aataacaatg gtaacttgtc cagaaggcct atcatcattc ctagtaggtg   5245

ggcacagagt aagagatatt aagaagcttc tgatgagtc atcatctagc gaaggccctg   5305

tgtagggctt tattatagga gttacattga cttctggggc attcaaaggt ctccctcctt   5365

atccatatct ctgtcatttt gcttctccag ccacgacaac acactttcct ctccaactgc   5425

tccctcccca ccaaaaaaga agaccctcta aaaggcaaag gaataaatat tcttagaagt   5485

aaattatctt catcccatgc tgccttttc aaagaggtgt taggatattt atcctatttc   5545

tgtatttcac agtagctttt caggctgtcc tgcttatata taagctgatt tatattgaga   5605

aaaatcactt ttgaataaag aggatgaaat gactttacac cccattaaat actcagtcaa   5665

gcttagccat gactcagtaa ctaaaaagtt caaaaaatcc agttatgtaa tgtgcagagt   5725

aacaaattgc aagaaaaaca acttaatctt ccagtgacta agtaagaaaa actgttgtca   5785

ctattaaaca tgtaggaaat tgataattat tacaaacaaa gcaatactct accctaaatc   5845

tagacaaatc actggacaga tgataagatt ttcagctttc tcctttaaag agctgtgcca   5905

atgtacagat ttttttgtaa acatgcaaag ggaaggttac aaactcctta aactttaaaa   5965

aaccataaat cctttctttg ctacttatat tctatgccaa ttataatatt ccaagactta   6025

cctttcttca gaatgcttac atatggaaag gtttatttat aaatatttga taggtaaata   6085

ttccatatgt attttctagc ccgtctttct ctgtccctcc ctcaaataac ttcattaccc   6145
```

```
tctccttttt aaacgaaata tcttgataat aagaaaacaa aatcattttt ttgtgaaata    6205

atacatatgg acaaaaaata caagttgtat tttacttctg gttcattaaa atattgtgtt    6265

tagttggatt ttttcctcct ttattttcag aaacataaaa gaaattgttt tatttcctaa    6325

aggataaaat tggatatagc ctctttagta gacactatca cagttctgtt gtttgctgtg    6385

ttcatttgct taatgaattg cgtgagaaca gtcactgtaa tgaaatatgt gtgctggggg    6445

tgggggaag ggcatgggaa atgtttatg aaaaaaagtt ataagcctaa tactatgaag    6505

taacatctaa tgcagttctt tttaagtgca atatatttat ttctgctaga aatatattat    6565

caaccttatg taatatttga agcattacat attatttgta aacagcttaa aattatatat    6625

taccccaatt gtacataagt acaaatgtgt ggatattagt ttctttcatt aaaagtggtg    6685

ttttttaaa aataaaaaaa aaaaaaaaa aa                                    6717
```

<210> 2
<211> 447
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Glu Phe Thr Ala Ser Pro Lys Pro Gln Leu Ser Ser Arg Ala Asn
1               5                   10                  15

Ala Phe Ser Ile Ala Ala Leu Met Ser Ser Gly Gly Ser Lys Glu Lys
            20                  25                  30

Glu Ala Thr Glu Asn Thr Ile Lys Pro Leu Glu Gln Phe Val Glu Lys
        35                  40                  45

Ser Ser Cys Ala Gln Pro Leu Gly Glu Leu Thr Ser Leu Asp Ala His
    50                  55                  60

Gly Glu Phe Gly Gly Gly Ser Gly Ser Ser Pro Ser Ser Ser Ser Leu
65                  70                  75                  80

Cys Thr Glu Pro Leu Ile Pro Thr Thr Pro Ile Ile Pro Ser Glu Glu
                85                  90                  95

Met Ala Lys Ile Ala Cys Ser Leu Glu Thr Lys Glu Leu Trp Asp Lys
                100                 105                 110

Phe His Glu Leu Gly Thr Glu Met Ile Ile Thr Lys Ser Gly Arg Arg
            115                 120                 125

Met Phe Pro Thr Ile Arg Val Ser Phe Ser Gly Val Asp Pro Glu Ala
        130                 135                 140

Lys Tyr Ile Val Leu Met Asp Ile Val Pro Val Asp Asn Lys Arg Tyr
145                 150                 155                 160

Arg Tyr Ala Tyr His Arg Ser Ser Trp Leu Val Ala Gly Lys Ala Asp
                165                 170                 175

Pro Pro Leu Pro Ala Arg Leu Tyr Val His Pro Asp Ser Pro Phe Thr
            180                 185                 190
```

```
Gly Glu Gln Leu Leu Lys Gln Met Val Ser Phe Glu Lys Val Lys Leu
        195             200             205
```

```
Thr Asn Asn Glu Leu Asp Gln His Gly His Ile Ile Leu Asn Ser Met
    210             215             220
```

```
His Lys Tyr Gln Pro Arg Val His Ile Ile Lys Lys Lys Asp His Thr
225             230             235             240
```

```
Ala Ser Leu Leu Asn Leu Lys Ser Glu Glu Phe Arg Thr Phe Ile Phe
            245             250             255
```

```
Pro Glu Thr Val Phe Thr Ala Val Thr Ala Tyr Gln Asn Gln Leu Ile
            260             265             270
```

```
Thr Lys Leu Lys Ile Asp Ser Asn Pro Phe Ala Lys Gly Phe Arg Asp
        275             280             285
```

```
Ser Ser Arg Leu Thr Asp Ile Glu Arg Glu Ser Val Glu Ser Leu Ile
    290             295             300
```

```
Gln Lys His Ser Tyr Ala Arg Ser Pro Ile Arg Thr Tyr Gly Gly Glu
305             310             315             320
```

```
Glu Asp Val Leu Gly Asp Glu Ser Gln Thr Thr Pro Asn Arg Gly Ser
            325             330             335
```

```
Ala Phe Thr Thr Ser Asp Asn Leu Ser Leu Ser Ser Trp Val Ser Ser
            340             345             350
```

```
Ser Ser Ser Phe Pro Gly Phe Gln His Pro Gln Ser Leu Thr Ala Leu
    355             360             365
```

```
Gly Thr Ser Thr Ala Ser Ile Ala Thr Pro Ile Pro His Pro Ile Gln
    370             375             380
```

```
Gly Ser Leu Pro Pro Tyr Ser Arg Leu Gly Met Pro Leu Thr Pro Ser
385             390             395             400
```

```
Ala Ile Ala Ser Ser Met Gln Gly Ser Gly Pro Thr Phe Pro Ser Phe
            405             410             415
```

```
His Met Pro Arg Tyr His His Tyr Phe Gln Gln Gly Pro Tyr Ala Ala
            420             425             430
```

```
Ile Gln Gly Leu Arg His Ser Ser Ala Val Met Thr Pro Phe Val
        435             440             445
```

```
<210>  3
<211>  387
<212>  PRT
<213>  Mus musculus

<400>  3
```

```
Met Glu Phe Thr Ala Ser Pro Lys Pro Gln Leu Ser Ser Arg Ala Asn
```

```
1                   5                    10                   15
Ala Phe Ser Ile Ala Ala Leu Met Ser Ser Gly Gly Pro Lys Glu Lys
            20                  25                  30
Glu Ala Ala Glu Asn Thr Ile Lys Pro Leu Glu Gln Phe Val Glu Lys
            35                  40                  45
Ser Ser Cys Ala Gln Pro Leu Gly Glu Leu Thr Ser Leu Asp Ala His
    50                  55                  60
Ala Glu Phe Gly Gly Gly Gly Gly Ser Pro Ser Ser Ser Ser Leu Cys
65                  70                  75                  80
Thr Glu Pro Leu Ile Pro Thr Thr Pro Ile Ile Pro Ser Glu Glu Met
            85                  90                  95
Ala Lys Ile Ala Cys Ser Leu Glu Thr Lys Glu Leu Trp Asp Lys Phe
            100                 105                 110
His Glu Leu Gly Thr Glu Met Ile Ile Thr Lys Ser Gly Arg Arg Met
            115                 120                 125
Phe Pro Thr Ile Arg Val Ser Phe Ser Gly Val Asp Pro Glu Ser Lys
    130                 135                 140
Tyr Ile Val Leu Met Asp Ile Val Pro Val Asp Asn Lys Arg Tyr Arg
145                 150                 155                 160
Tyr Ala Tyr His Arg Ser Ser Trp Leu Val Ala Gly Lys Ala Asp Pro
            165                 170                 175
Pro Leu Pro Ala Arg Leu Tyr Val His Pro Asp Ser Pro Phe Thr Gly
            180                 185                 190
Glu Gln Leu Leu Lys Gln Met Val Ser Phe Glu Lys Val Lys Leu Thr
            195                 200                 205
Asn Asn Glu Leu Asp Gln His Gly His Ile Asp Ser Asn Pro Phe Ala
    210                 215                 220
Lys Gly Phe Arg Asp Ser Ser Arg Leu Thr Asp Ile Glu Arg Glu Ser
225                 230                 235                 240
Val Glu Ser Leu Ile Gln Lys His Ser Tyr Ala Arg Ser Pro Ile Arg
            245                 250                 255
Thr Tyr Gly Glu Glu Asp Val Leu Gly Glu Glu Ser Gln Thr Thr Gln
            260                 265                 270
Ser Arg Gly Ser Ala Phe Thr Thr Ser Asp Asn Leu Ser Leu Ser Ser
            275                 280                 285
Trp Val Ser Ser Ser Ser Ser Phe Pro Gly Phe Gln His Pro Gln Pro
    290                 295                 300
Leu Thr Ala Leu Gly Thr Ser Thr Ala Ser Ile Ala Thr Pro Ile Pro
305                 310                 315                 320
His Pro Ile Gln Gly Ser Leu Pro Pro Tyr Ser Arg Leu Gly Met Pro
            325                 330                 335
Leu Thr Pro Ser Ala Ile Ala Ser Ser Met Gln Gly Ser Gly Pro Thr
            340                 345                 350
Phe Pro Ser Phe His Met Pro Arg Tyr His His Tyr Phe Gln Gln Gly
            355                 360                 365
Pro Tyr Ala Ala Ile Gln Gly Leu Arg His Ser Ser Ala Val Met Thr
    370                 375                 380
Pro Phe Val
385
```